

Figure 1A

1	CCACTGTGCTGGAATTCGGCACGAGGCGAACGGACGTTTAAAGTGAGAAAAGAAACCGG	60
61	TAAATCAGAGATCCCAAGCAAGCGCGTGCATGATAGCGAAGAAAAAAGCTATCCG	120
121	TTTCAGTTAACTACTTACCAAGATTGAATTCGCCATCGGGCAAATTACTAAAAATACAT	180
181	AAGTGCAACTCGTCCACTGTGTGTTGTGTTTTTTTTTTTTTTTGGTTTTCGCTGTGCC	240
241	TTTATCGCAAACAAGAACTGATAAACTAGAAAATATCTTGAGAAACTTGTTTTTCGCGCT	300
301	TTTCTTTTGCTAATTGCCGATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTG	360
361	GTAATACAATCTGAAAAGGGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTGC	420
421	CAGCTTATCATCTCATGCTGTCTGTGAGGTTGTTCTGTGTGCTCGTGTAGTATCTTAAAT	480
481	ACATAGAGTGTGTTTCATATAAAGTGCGACAAAGCTCGATTGGAAACAGCTGTCGAGTGCC	540
541	CTTGAGTGGGTGGGCAAGATCGTCATCATCATCATCGTCGTCATTATCAACAGAATCAGC	600
601	ATCAGCATCTGGAGGCCCCGGATGCTCTAAGATCCCCAGTGTTTCATCAATTATGACTGCC	660
1		3
	<u>M T A</u>	
661	GAGACCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTTCCGGCCAAA	720
4	<u>E T L K P F I T P T S A N D D G F P A K</u>	23
721	GCGACCAGCACGGCGACCGCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTGGGG	780
24	<u>A T S T A T A Q R R T R Q L I P L V L G</u>	43
781	TTCATCGGTCTGGGGCTGGTTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGT	840
44	<u>F I G L G L V V A I L A L T I W Q T T R</u>	63
841	GTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAG	900
64	<u>V S H L D K E L K S L K R V V D N L Q Q</u>	83
901	CGTTTGGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCC	960
84	<u>R L G I N Y L D E F D E F Q K E Y E N A</u>	103
961	CTCATCGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGC	1020
104	<u>L I D Y P K K V D G L T D E E D D D D G</u>	123

Figure 1B

1021	GATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGAT	1080
124	D G L D S I A D D E D D D V S Y S S V D	143
1081	GATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAACAATGCACAT	1140
144	D V G A D Y E D Y T D M L N K L N N A H	163
1141	ACCGGCACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCA	1200
164	T G T T P T S E T T A E G E G E T D S A	183
1201	TCCTCAGCCTCAAATGATGACAATGTGTTTCGATGACTTTACCAGCTCAGATGCCCTCAAA	1260
184	S S A S N D D N V F D D F T S S D A L K	203
1261	AAGAAGCAGGAGAGAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATT	1320
204	K K Q E R K S R S I A D V R N E E Q N I	223
1321	CAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAGCTTCCAAAGAGAGC	1380
224	Q G N H T E L Q E K S S N E A A S K E S	243
1381	CCTGCAGCACTTCACCTCCGTCGCAGAATGCATTCCCGCCATCGCCACCTCGTAGTCCGC	1440
244	P A A L H L R R R M H S R H R H L V V R	263
1441	AAAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCATTTCCACTTGAGCAGCAGGCGGCGT	1500
264	K A R S E D S R P A A H F H L S S R R R	283
1501	CACCAAGAAAGTATGGGCTACCATGGAGATATGTACATAGAAAATGATAGGGAGAGATGC	1560
284	H Q E S M G Y H G D M Y I E N D R E R C	303
1561	TCTTATCAGGGACACTTTCAAACGCGCGATGGCGTATTGACGGTGACCAATGCAGGCCTA	1620
304	S Y Q G H F Q T R D G V L T T V C T N A G I L	323
1621	TATTACGTATACGCCCAGATATGGGGCTACAACTCGCACGACCAGAACGGATTTATCGTC	1680
324	Y Y V Y A Q I W G Y N S H D Q N G F I V	343
1681	TTTCAAGGAGACACTCCATTCCCTGCAGTGCTTGAACACGGTGCCCAACATGCCACAT	1740
344	F Q G D T P F L Q C L N T V P T N M P H	363
1741	AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCAT	1800
364	K V H T C H T S G L I H L E R N E R I H	383
1801	CTGAAGGACATTCAACAACGATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTAC	1860
384	L K D I H N D R N A V L R E G N N R S Y	403

[illegible][illegible]

Figure 2A

1	ATGACTGCCGAGACCCCTCAAGCCGTTTATAACGCCAACGAGTGCCAACGATGATGGTTTT	60
1	M T A E T L K P F I T P T S A N D D G F	20
61	CCGGCCAAAGCGACCAGCACGGCGACCGCCCAGCGACGCACCCGCCAGCTGATCCCCCTG	120
21	P A K A T S T A T A Q R R T R Q L I P L	40
121	GTTTTGGGGTTCATCGGTCTGGGGCTGGTCGTTGCCATTCTCGCACTAACGATCTGGCAG	180
41	V L G F I G L G L V V A I L A L T I W Q	60
181	ACAACGCGTGTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAAT	240
61	T T R V S H L D K E L K S L K R V V D N	80
241	CTCCAGCAGCGTTTGGGCATAAACTATCTGGACGAGTTTCGACGAGTTCCAAAAGGAGTAC	300
81	L Q Q R L G I N Y L D E F D E F Q K E Y	100
301	GAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGAC	360
101	E N A L I D Y P K K V D G L T D E E D D	120
361	GACGATGGCGATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGC	420
121	D D G D G L D S I A D D E D D D V S Y S	140
421	TCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAAC	480
141	S V D D V G A D Y E D Y T D M L N K L N	160
481	AATGCACATACCGGCACCACGCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACG	540
161	N A H T G T T P T S E T T A E G E G E T	180
541	GACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTTCGATGACTTTACCAGCTACAAT	600
181	D S A S S A S N D D N V F D D F T S Y N	200
601	GCCCCAAAAAGAAGCAGGAGAGAAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAG	660
201	A H K K K Q E R K S R S I A D V R N E E	220
661	CAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACTTCC	720
221	Q N I Q G N H T E L Q E K S S N E A T S	240
721	AAAGAGAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGGTGAATCTCTTCTT	780
241	K E R M H S R H R H L L V R K G E S L L	260
781	TCAGCCAGATCCGAGGACTCGAGGCCAGCAGCCATTTCCTTGGAGCAGCAGGCGGCGT	840
261	S A R S E D S R P A A H F H L S S R R R	280
841	CACCAAGGAAGTATGGGCTACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAAC	900
281	H Q G S M G Y H G D M Y I G N D N E R N	300

Figure 2B

901 TCTTATCAGGGACACTTTCAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTA 960
301 S Y Q G H F Q T R D G V L T V T N T G I 320

961 TATTACGTATACGCCCAGATATGCTACAACAACTCGCACGACCAGAACGGATTTATCGTC 1020
321 V Y V Y A Q I C Y N N S H D Q N G F I V 340

1021 TTTCAAGGAGACACTCCATTTCCTGCAGTGCTTGAACACGGTGCCACCAACATGCCACAT 1080
341 F Q G D T P F L Q C L N T V P T N M P H 360

1081 AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCAT 1140
361 K V H T C H T S G L I H L E R N E R I H 380

1141 CTGAAGGACATTCAACAACGATCGCAATGCAGTTCTGCGGGAGGGAAAACAACCGAAGCTAC 1200
381 L K D I H N D R N A V L R E G N N R S Y 400

1201 TTTGGCATCTTCAAGGTGTAA 1221
401 F G I F K V 406

Figur 3A

1	GGCACGAGGCGAACGGACGTTTAAAGTGAGAAAAGAAACCGGTAAATCAGAGATCCCAAG	60
61	CAAGCGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTTAC	120
121	CAAGATTGAATTTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACT	180
181	GTGTGTTGTGTTTTTTTTTTTTTTTTTGGTTTTTCGCTGTGCCTTTATCGCAAACAAGAAC	240
241	TGATAAAACTAGAAAATATCTTGAGAAACTTGTTTTTCGCGCTTTTCTTTTGCTAATTGCC	300
301	GATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAG	360
361	GGCACCATCAGCAGCCCGAGGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGC	420
421	TGTCTGTGAGGTGTTCTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTTATA	480
481	TAAAGTGCGACAAAGCTCGATTGGAAACAGCTGTGAGTGCCTTGAGTGGGTGGGCAAG	540
541	ATCGTCATCATCATCATCGTCGTCATTATCAACAGAATCAGCATCAGCATCTGGAGGCC	600
601	CGGTTGCTCTAAGATCCCCAGTGTTTCATCAATTATGACTGCCGAGACCTCAAGCCGTTT	660
1	<u>M T A E T L K P F</u>	9
661	ATAACGCCAACGAGTGCCAACGATGATGGTTTTCCGGCCAAAGCGACCAGCACGGCGACC	720
10	<u>I T P T S A N D D G F P A K A T S T A T</u>	29
721	GCCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTTTGGGGTTCATCGGTCTGGGGCTG	780
30	<u>A Q R R T R Q L I P L V L G F I G L G L</u>	49
781	GTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGTGTATCGCATCTGGACAAG	840
50	<u>V V A I L A L T I W Q T T R V S H L D K</u>	69
841	GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGGGCATAAACTAT	900
70	E L K S L K R V V D N L Q Q R L G I N Y	89
901	CTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAA	960
90	L D E F D E F Q K E Y E N A L I D Y P K	109
961	AAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTCTGGATTCCATT	1020
110	K V D G L T D E E D D D D G D G L D S I	129

Figur 3B

1021	GCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTAC	1080
130	A D D E D D D V S Y S S V D D V G A D Y	149
1081	GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCCACA	1140
150	E D Y T D M L N K L N N A H T G T T P T	169
1141	TCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCATCCTCAGCCTCAAATGAT	1200
170	S E T T A E G E G E T D S A S S A S N D	189
1201	GACAATGTGTTTCGATGACTTTACCAGCTACAATGCCACAAAAAGAAGCAGGAGAGAAAA	1260
190	D N V F D D F T S Y N A H K K K Q E R K	209
1261	TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAATCACACAGAG	1320
210	S R S I A D V R N E E Q N I Q G N H T E	229
1321	CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGCCCTGCACCACTTCACCAC	1380
230	L Q E K S S N E A T S K E S P A P L H H	249
1381	CGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCAGATCCGAGGAC	1440
250	R R R M H S R H R H L L V R K A R S E D	269
1441	TCGAGGCCAGCAGCCCCATTTCCACTTGAGCAGCAGGCGGCGTCACCAAGGAAGTATGGGC	1500
270	S R P A A H F H L S S R R R H Q G S M G	289
1501	TACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTT	1560
290	Y H G D M Y I G N D N E R N S Y Q G H F	309
1561	CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAG	1620
310	Q T R D G V L T V I T N T G L Y Y W Y A I C	329
1621	ATATGCTACAACAACCTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCA	1680
330	E Q Y N N S H D Q N G F I V F Q G D T P	349
1681	TTCCTGCAGTGCTTGAACACGGTGCCCACCAACATGCCACATAAGGTGCACACCTGCCAC	1740
350	F L Q C L N T V P T N M P H K V H T C H	369
1741	ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCATCTGAAGGACATTCAACAAC	1800
370	T S G L I H L E R N E R I H L K D I H N	389
1801	GATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG	1860
390	D R N A V L R E G N N R S Y F G I F K V	409
1861	TAAATTGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAGTTTAAGCTTTTGTCCCCG	1920

Figure 3C

1921 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1980
1981 TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGG 2040
2041 AGGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAAATATA 2100
2101 TGTAGCTATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAG 2148

1921 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1980
1981 TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGG 2040
2041 AGGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAAATATA 2100
2101 TGTAGCTATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAG 2148

Figur 4

		1	50
DmTNF	(1)	MTAETLKPFITPTSANDDGFPKATSTATAQRRTRQLIPLVLGFIGLGLV	
DmTNFv1	(1)	MTAETLKPFITPTSANDDGFPKATSTATAQRRTRQLIPLVLGFIGLGLV	
DmTNFv2	(1)	MTAETLKPFITPTSANDDGFPKATSTATAQRRTRQLIPLVLGFIGLGLV	
		51	100
DmTNF	(51)	VAILALTIWQTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
DmTNFv1	(51)	VAILALTIWQTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
DmTNFv2	(51)	VAILALTIWQTRVSHLDKELKSLKRVVDNLQORLGINYLDEFDEFQKEY	
		101	150
DmTNF	(101)	ENALIDYPKKVDGLTDEEDDDGGLDSIADDEDDVSYSSVDDVGADYE	
DmTNFv1	(101)	ENALIDYPKKVDGLTDEEDDDGGLDSIADDEDDVSYSSVDDVGADYE	
DmTNFv2	(101)	ENALIDYPKKVDGLTDEEDDDGGLDSIADDEDDVSYSSVDDVGADYE	
		151	200
DmTNF	(151)	DYTDMLNKLNNNAHTGTTPTSETTAEGETDSASSASNDNDVDFDFTSS	
DmTNFv1	(151)	DYTDMLNKLNNNAHTGTTPTSETTAEGETDSASSASNDNDVDFDFTSYN	
DmTNFv2	(151)	DYTDMLNKLNNNAHTGTTPTSETTAEGETDSASSASNDNDVDFDFTSYN	
		201	250
DmTNF	(201)	AHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEAASKESPAALHLR	
DmTNFv1	(201)	AHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEAASKESPAALHLR	
DmTNFv2	(201)	AHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEAASKESPAALHLR	
		251	300
DmTNF	(251)	RRMHSRHRHLVVRK-----ARSEDSRPAAHFHLSSRRRHQESMGYHGDM	
DmTNFv1	(243)	RRMHSRHRHLVVRKGESLLSARSEDSRPAAHFHLSSRRRHQESMGYHGDM	
DmTNFv2	(251)	RRMHSRHRHLVVRK-----ARSEDSRPAAHFHLSSRRRHQESMGYHGDM	
		301	350
DmTNF	(295)	YIENDNERNSYQGHFQTRDGVLTVTNAGLYYVYAQICYNNSHDQNGFIVF	
DmTNFv1	(292)	YIENDNERNSYQGHFQTRDGVLTVTNAGLYYVYAQICYNNSHDQNGFIVF	
DmTNFv2	(295)	YIENDNERNSYQGHFQTRDGVLTVTNAGLYYVYAQICYNNSHDQNGFIVF	
		351	400
DmTNF	(345)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHCLKDIHNDRNAV	
DmTNFv1	(342)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHCLKDIHNDRNAV	
DmTNFv2	(345)	QGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHCLKDIHNDRNAV	
		401	415
DmTNF	(395)	LREGNNRSYFGIFKV	
DmTNFv1	(392)	LREGNNRSYFGIFKV	
DmTNFv2	(395)	LREGNNRSYFGIFKV	

Figure 5

AC005974 : DS05033 (P1 D347), DS01913 (P1 D350). Finished; 158983 bases.
Length = 158,983

Minus Strand HSPs:

Score = 77 (27.1 bits), Expect = 5.5, P = 1.0
Identities = 20/58 (34%), Positives = 31/58 (53%), Frame = -1

Query: 203 NGKLIVNQDGFYYLYANICFRH-HETSGDLA---TEYLQLMVYV-TKTSIKIPSSHT 254
+G L V G YY+YA IC+ + H+ +G + T +LQ + V T K+ + HT
Sbjct: 129394 DGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHT
129221

Score = 45 (15.8 bits), Expect = 79., Sum P(2) = 1.0
Identities = 9/17 (52%), Positives = 10/17 (58%), Frame = -1

Query: 28 GPLHAPP--PPAPHQPP 42
GP PP PP+P PP
Sbjct: 132361 GPSLPPFPFPPSPRTTP 132311

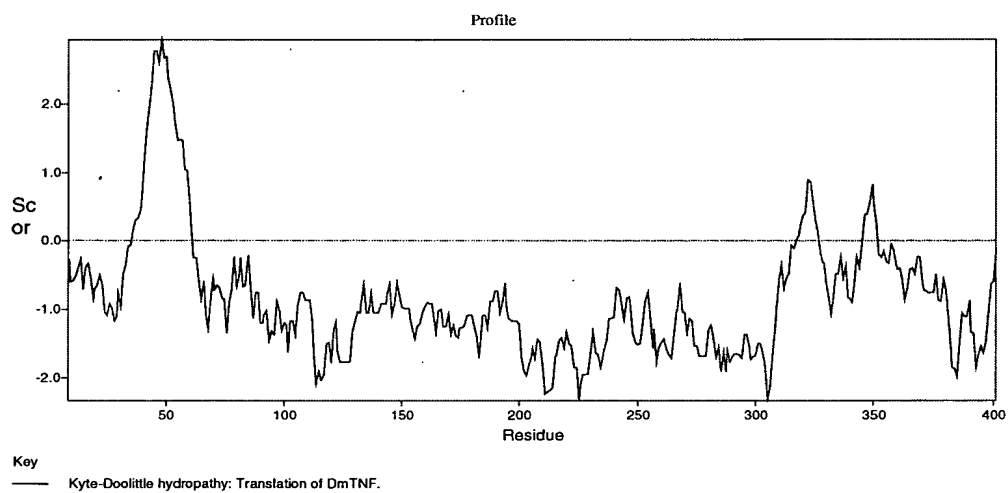
129394 DGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHT 129221

[illegible]

Figur 6B

		301		350
DmTNF	(272)	PAAHFHLSSRRRHQESMGYHCDMYIENDRER-CSYQGHQOTRDGVLTVTN		
DmTNFv1	(269)	PAAHFHLSSRRRHQESMGYHCDMYIENDRER-NSYQGHQOTRDGVLTVTN		
DmTNFv2	(272)	PAAHFHLSSRRRHQESMGYHCDMYIENDRER-NSYQGHQOTRDGVLTVTN		
Osteoprotegerin	(165)	--FAHLTINATDIPSG-SHKVSLSSWYHARG-WAKLSNMTFSNCKLIVNQ		
hCD27L	(53)	--LGWDVDELQLNHTGPPQDPRIYWQGGPALGRSELHGPELDKCOLRTHR		
hCD30L	(86)	LLCILKRAPPFKKSWAYLQVAKHINKTKLSWNKDELLHGVRYPQDGNLVITQF		
hTRAIL	(131)	-GRSN-TLSSPNSKNEKALGRKINSWESSRSGHSFLSNHILRNCELVIHE		
hEctodysplasmin_A	(249)	AVVHLQGGGSAIQVKNDLSGCVINDWSRITM-NEKMFKLHPRSGELEVLV		
mEctodysplasmin_A	(249)	AVVHLQGGGSAIQVKNDLSGCVINDWSRITM-NEKMFKLHPRSGELEVLV		
		351		400
DmTNF	(321)	AGLYYYVY-----AQHWGYNSHDONGEIVEFG-DTPFLQCLNTVPTNM		
DmTNFv1	(318)	TGLYYVYV-----AQHCYNNSHDONGEIVEFG-DTPFLQCLNTVPTNM		
DmTNFv2	(321)	TGLYYVYV-----AQHCYNNSHDONGEIVEFG-DTPFLQCLNTVPTNM		
Osteoprotegerin	(211)	DGFYYEYANICFRHHETSGDLATEYLLQMVVYTKTSIKHPSSTHLMKGGGS		
hCD27L	(101)	DGLYMHVITVTLAICSSITASRHHPTLLAVGTCSS--PASSISLRLSF		
hCD30L	(136)	PGLYFTICQLQFLVQCPNNSVDLKELELLINKHIKKQALVTVCESGMOTKH		
hTRAIL	(179)	KGEYYIYSCOTYFRFQEEIKENIKNDKQMVQYIYK-YTGYPPDILLMK SAR		
hEctodysplasmin_A	(298)	DGTVEIYISO-----VEVYYINFTDFASVEVVVD-EKPFLOCTRSTETGK		
mEctodysplasmin_A	(298)	DGTVEIYISO-----VEVYYINFTDFASVEVVVD-EKPFLOCTRSTETGK		
		401		450
DmTNF	(362)	PHK-----VHTCHTSGLIHLEARNERIHLEKDIHNDRNAVLREGNNRSY		
DmTNFv1	(359)	PHK-----VHTCHTSGLIHLEARNERIHLEKDIHNDRNAVLREGNNRSY		
DmTNFv2	(362)	PHK-----VHTCHTSGLIHLEARNERIHLEKDIHNDRNAVLREGNNRSY		
Osteoprotegerin	(261)	TKYWSGNSEPHFYVSINVCGEFKLRSGEETSTEVSINPSILDPDQ---DATY		
hCD27L	(148)	HQG-----CTIVSORLTPLARGDTLCTNLGTLLPSRNT---DETF		
hCD30L	(186)	VYQN-----LSQFLDYLQVNTTISVNVDTFYIDTSTFPLENVL		
hTRAIL	(228)	NSCWSKDAEYGLYSIVQCGTFELKENDRIFVSVTNEHLIDMDH---EASE		
hEctodysplasmin_A	(341)	TN-----YNTCYTAGVCLLKAROKIAVKMVHADISINMS--KHTTF		
mEctodysplasmin_A	(341)	TN-----YNTCYTAGVCLLKAROKIAVKMVHADISINMS--KHTTF		
		451		462
DmTNF	(404)	FGIFKV-----		
DmTNFv1	(401)	FGIFKV-----		
DmTNFv2	(404)	FGIFKV-----		
Osteoprotegerin	(308)	FGAFKVRDID--		
hCD27L	(186)	FGVQWVRP----		
hCD30L	(226)	SIFEYSNSD----		
hTRAIL	(275)	FGAFLVG-----		
hEctodysplasmin_A	(380)	FGAFLRGEAPAS		
mEctodysplasmin_A	(380)	FGAFLRGEAPAS		

Figure 7



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Figure 8

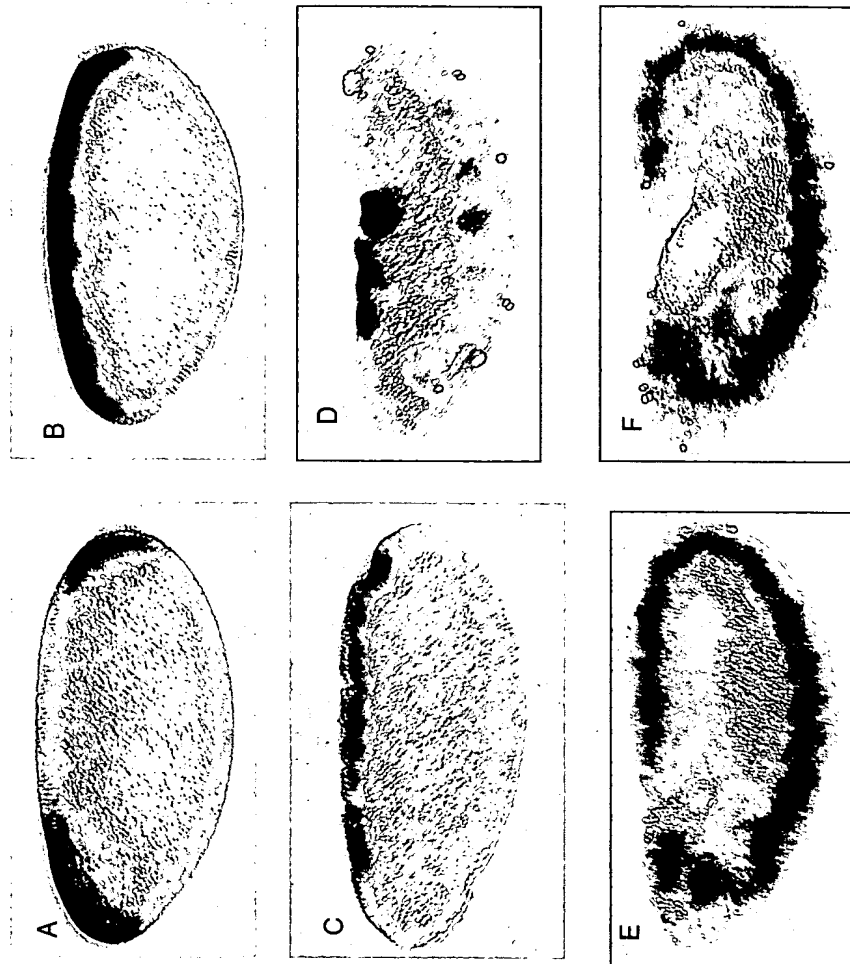


Figure 9

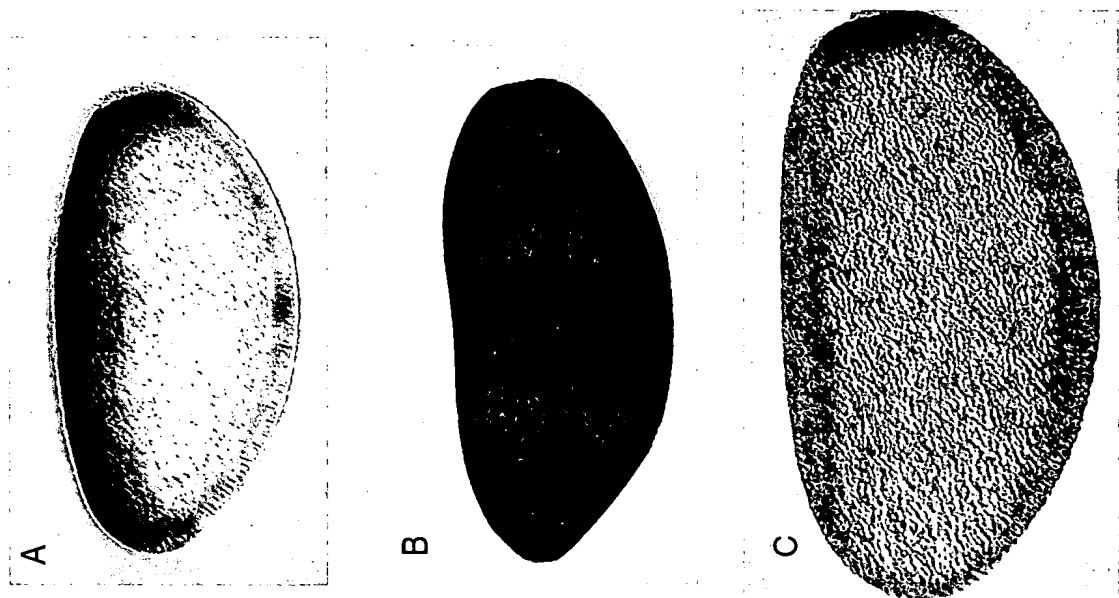


Figure 10

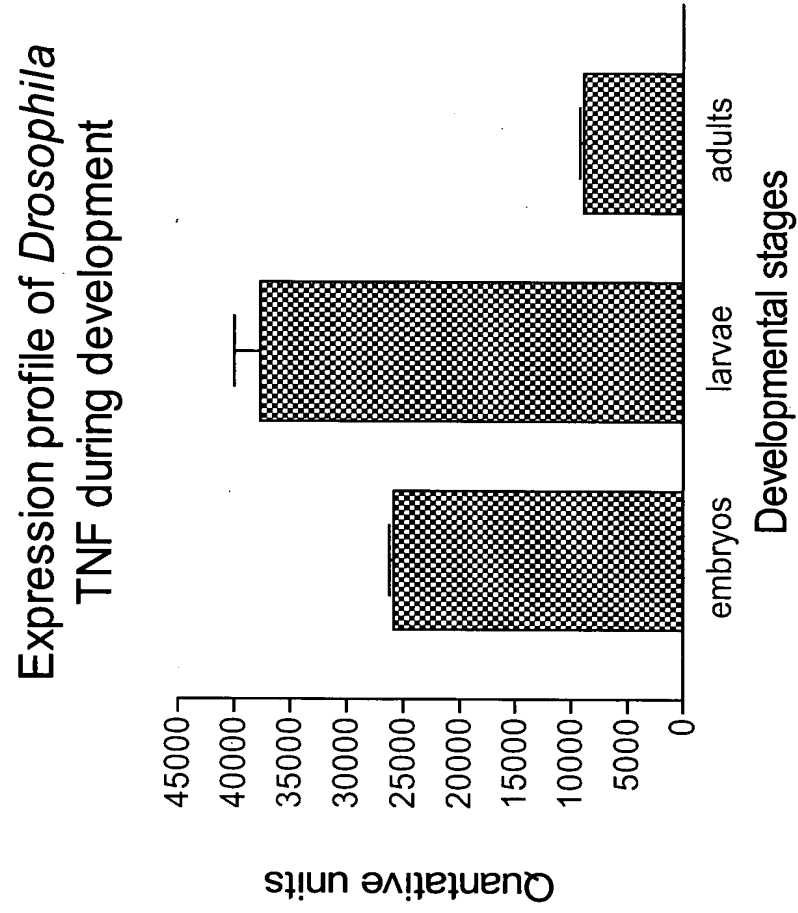


Figure 11

DmTNF

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.6%	34.4%
human ectodysplasmin_A protein	gilQ92838	21.2%	27.9%
mouse ectodysplasmin_A protein	gilNP_034229	20.4%	28.5%

DmTNFv1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	23.8%	30.5%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	23.3%	32.7%
human ectodysplasmin_A protein	gilQ92838	21.8%	28.6%
mouse ectodysplasmin_A protein	gilNP_034229	21%	28.6%

DmTNFv2

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.1%	33.9%
human ectodysplasmin_A protein	gilQ92838	22.4%	29.1%
mouse ectodysplasmin_A protein	gilNP_034229	21.6%	29.2%

Figure 12

S-dmTNF

